

10/643,589
Sequence alignment B
US-08-633-148-2
; Sequence 2, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-2

Query Match 84.6%; Score 1807; DB 1; Length 340;
Best Local Similarity 99.7%; Pred. No. 4.3e-138;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MAAGTAVGAWVLVLSLWGAVVGAQNITARIGEPLVLKCKGAPKKPPQRLEWKLNTGRTEA	60
Db	1	MAAGTAVGAWVLVLSLWGAVVGAQNITARIGEPLVLKCKGAPKKPPQRLEWKLNTGRTEA	60
Qy	61	WKVLSPQGGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETHSNYRVRVYQI	120
Db	61	WKVLSPQGGGPWDSVARVLPNGSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRVYQI	120
Qy	121	PGKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH	180
Db	121	PGKPEIVDSASELTAGVPNKVGTCTVSEGSYPAGTILSWHLDGKPLVPNEKGVSVKEQTRRH	180
Qy	181	PETGLFTLQSELMTVPARGGDPRTFSCSFSPGLPRHRALRTAPIQPRVWEPVPLEEVQL	240
Db	181	PETGLFTLQSELMTVPARGGDPRTFSCSFSPGLPRHRALRTAPIQPRVWEPVPLEEVQL	240
Qy	241	VVEPEGGAVAPGGTIVTLTCEVPAQPSPIHWMKDGVPPLPPSPVLILPEIGPDQGTYS	300
Db	241	VVEPEGGAVAPGGTIVTLTCEVPAQPSPIHWMKDGVPPLPPSPVLILPEIGPDQGTYS	300
Qy	301	CVATHSSHGFPQESRAVSISIIIEPGEEGPTAGSVGGSGGLGT	340
Db	301	CVATHSSHGFPQESRAVSISIIIEPGEEGPTAGSVGGSGGLGT	340